- Biomarkers
- Definition:

A biomarker is ‘a characteristic that is objectively measured and evaluated as an indicator of normal biological processes, pathogenic processes, or pharmacologic responses to a therapeutic intervention’.

A characteristic that is objectively measured and evaluated as an indicator of healthy biological processes, pathological processes, or pharmacological responses to therapeutic intervention

- Example:
    1. An antibody
    2. Blood pressure
    3. Cardiovascular markers
    4. Insulin (UT)
- Types:
  • Diagnostic
  • Early detection
  • Monitoring
  • Prognostic
  • Predictive/Safety/dose

Types:

Diagnostic:

Diagnostic biomarkers are used to make predictions on patients suspected of having the disease

• Temperature

• Bacterial tests (streptococcal)

• Origin of cancer tissue

Screening:

Screening biomarkers are used to predict the potential occurrence of a disease in asymptomatic patients.

• Gene test for monogenic diseases (like

cystic fibrosis)

• PSA (still controversial)

• Breast cancer screening

Prognostic:

Prognostic biomarkers are applied to predict the outcome of a patient suffering from a disease.

• Mammaprint: 70 gene expression to split breast cancer patients into high vs. low risk of metastases

Homozygous and Heterozygous

If a given pair consists of similar genes, the individual is said to be **homozygous** for the gene in question, while if the genes are dissimilar, the individual is said to be **heterozygous.** For example, if we have two alternative genes, say *A* and *a*, there are two kinds of **homozygotes**, namely *AA* and *aa*, and one kind of **heterozygote**, namely *Aa*. Genes are present in pairs in all cells of an adult organism, except for gametes. *That is, the gametes have only one gene from any given pair.* Thus if an adult has genotype *AA*, all the gametes produced are of type *A.* But if the genotype is *Aa*, two types of gametes are possible, *A* and *a*, and these are normally produced in equal numbers.

5.

Genotypes :

At each locus (except for sex chromosomes) there are 2 genes. These constitute the individual's ***genotype*** at the locus.

Phenotypes:

The expression of a genotype is called a ***phenotype***.

For example, hair color, weight, height, the presence or absence of a disease, etc.

Single Nucleotide Polymorphism (SNP)

A single nucleotide polymorphism (SNP) is a site in the genome where the DNA sequences of many individuals differ by a single A, T, C, or G.

Example:

two sequenced DNA fragments from different individuals, …ACACCCTA and …ACACCTTA, contain a difference in a single nucleotide. In this case, two nucleotides that make the two individuals different are C and T, which are called two alleles.

7.

Marker Analysis:

Genetic markers are polymorphic genetic sequences, like RFLPs or microsatellites, that differ within chromosomal alleles. Rather than analysing the sequence directly, this gene is inferred through analysis of a genetic marker. Marker analysis approach is quite helpful in population biology and ecology studies that can be trace patterns in populations like plants, animals, humans, etc.

Aim of marker analysis:

One of the most important aims of these marker analyses is to provide ordered hallmarks on chromosomes with which one can map functional quantitative trait loci (QTLs) determining complex phenotypic variation to particular genomic regions. The genomewide identification of QTLs, their locations and effects, is of fundamental importance for agricultural, evolutionary, and biomedical genetics.

6.

QTL Analysis:

Quantitative trait locus (QTL) analysis is a statistical method that links two types of information—phenotypic data (trait measurements) and genotypic data (usually molecular markers)—in an attempt to explain the genetic basis of variation in complex traits. QTL analysis allows researchers in fields as diverse as agriculture, evolution, and medicine to link certain complex phenotypes to specific regions of chromosomes. The goal of this process is to identify the action, interaction, number, and precise location of these regions.

14.

R packages use in GWAS:

1. gap
2. tdhap
3. powerpkg
4. hapassoc
5. haplo.ccs
6. haplo.stats
7. ldDesign
8. Ldheatmap
9. mapLD
10. pbatR
11. GenABEL
12. SNPassoc